

**Answers will be posted Tue, Jan 19**

**1.** Describe the series of steps that you would perform to isolate arginine-requiring mutants from a wild-type haploid yeast strain.

**2.** From problem 1 you identified 8 arginine-requiring mutants (*arg*) from an **a** mating type and 8 *arg* mutants from an  $\alpha$  mating type. All of the *arg* mutations are recessive. You cross all the **a** mating type mutants to all of the  $\alpha$  mating type mutants and analyze the resulting diploids for growth on plates lacking arginine. The results are shown below, where “+” means growth without arginine and “-“ means no growth without arginine.

	$\alpha$ 9	$\alpha$ 10	$\alpha$ 11	$\alpha$ 12	$\alpha$ 13	$\alpha$ 14	$\alpha$ 15	$\alpha$ 16
a 1	+	+	-	-	+	+	+	+
a 2	-	-	+	+	+	-	-	+
a 3	+	+	+	+	+	+	+	+
a 4	-	-	+	+	+	-	-	+
a 5	+	+	-	-	+	+	+	+
a 6	+	+	+	+	+	+	+	-
a 7	+	+	+	+	-	+	+	+
a 8	+	+	+	+	-	+	+	+

**2a.** How many different genes did you find among your mutations?

**2b.** Which mutations affect which genes? (Come up with a naming scheme for the genes and assign the numbered alleles to them.)

**3.** You are studying aging in fruit flies and have generated a number of homozygous long-lived fly mutants. You now wish to determine how many genes these six mutants represent and you perform pairwise crosses with all of the homozygous mutants. Results of this analysis are shown in the table below (where the intersection represents the phenotype of the offspring resulting from a particular cross):

	Mut 1	Mut 2	Mut 3	Mut 4	Mut 5	Mut 6	WT
Mut 1	-	+	-	-	+	+	+
Mut 2		-	+	+	+	-	+
Mut 3			-	-	+	+	+
Mut 4				-	+	+	+
Mut 5					-	+	+
Mut 6						-	+

+ indicates all offspring have normal lifespan.

- indicates all offspring are long-lived.

WT = a wild type strain of flies.

**3a.** Are these mutations dominant or recessive? How do you know?

**3b.** How many complementation groups do these mutations represent?

**3c.** Describe which mutations fall into each complementation group.

In addition to the long-lived fly mutants described above, you have also isolated two additional long-lived mutants (Mut 7 and Mut 8) that exhibit an unusual complementation pattern with respect to your other long-lived mutants, as shown below:

	Mut 1	Mut 2	Mut 3	Mut 4	Mut 5	Mut 6	WT
Mut 7	-	-	-	-	-	-	-
Mut 8	+	-	+	+	-	-	+

+ indicates all offspring have normal lifespan.

- indicates all offspring are long-lived.

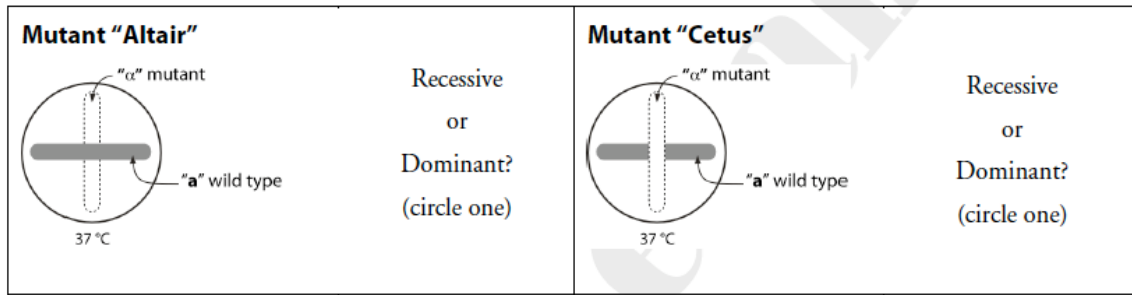
WT = a wild type strain of flies.

**3d.** What can you conclude from the results of crosses with Mut 7 and Mut 8?

**4.** Several temperature-sensitive mutant yeast strains have been isolated (named “Altair”, Cetus”, “Corvus”, and “Orion”). These haploid yeast strains all grow normally at 23°C but at 37°C, they all show premature separation of sister chromatids following DNA replication.

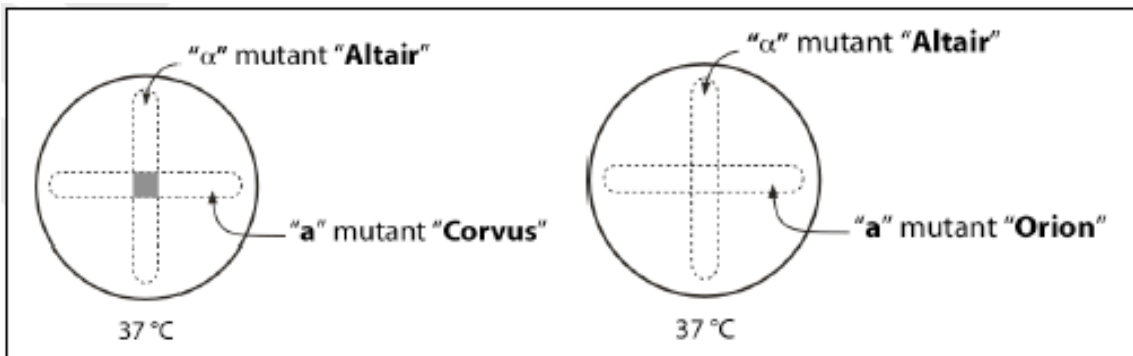
(a) Each mutant was tested as follows: mutant cells of mating type “α” were cross-stamped on a “complete” plate with wild type “a” mating type cells and tested for growth

at 37°C. The results are depicted below (where shading within each plate indicates growth). State whether each mutation is behaving as a recessive or dominant mutation, and explain how you know:

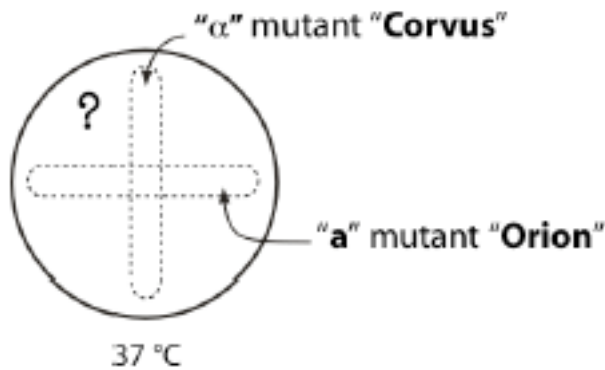


What led you to your conclusions?

(b) In a new test, Altair was cross-stamped with "Corvus" or with "Orion" as shown below. What do you conclude from these data? [Assume that Corvus and Orion gave exactly the same results as Altair when tested as in question 3(a).]



Predict the result of a cross between "Corvus" and "Orion" at 37 °C by shading where appropriate and if necessary in the diagram below:



(c) Mutants Altair and Corvus were mated to each other to form diploid cells, which were then allowed to undergo meiosis and form spores. Give the relevant genotypes of Altair and Corvus, the diploid, and the genotypes expected for the resulting spores. Use **E** / **e** as alleles designations if you think both strains are mutated in the same gene. Use **E** / **e** and **F** / **f** as allele designations and assume independent assortment if you think the two strains are mutated in different genes.

Altair's genotype:

Diploid's genotype:

Spore genotypes:

Corvus' genotype:

**5.** There are seven genes in yeast involved in synthesizing the amino acid histidine, called HIS1 through HIS7. To keep things simple, consider loss of function mutations affecting three of the genes, HIS1, HIS2, and HIS3. You have isolated mutations in each gene as follows:

HIS1 alleles: h1, h3, h6

HIS2 alleles: h2, h4

HIS3 allele: h5

Fill in the following phenotype table, which represents complementation tests for crosses among all of these mutations:

	h1	h2	h3	h4	h5	h6
h1						
h2						
h3						
h4						
h5						
h6						